

Appl. No. : 10/035,978
Filed : December 21, 2001

REMARKS

In response to the restriction requirement set forth in the communication, Applicant elects to prosecute Group II, Claims 4, 9-10, 14, and 20-23, drawn to nucleic acid probes, primers and oligonucleotides, classified in Class 536, subclass 23.1, for example. Note that Applicant intends to request rejoinder of the method claims of Group I, upon indication of allowable subject matter for the Group II claims.

In response to the election of species requirement, Applicants elect SEQ ID NO: 126 in order to be fully responsive to the restriction/election of species requirement. Claim 14 reads upon the elected species. This election is made with traverse. The traversal is set forth below.

The Examiner asserts that the claims are drawn to require numerous primers and probes and requires selection of a pair of primer and probe for method claims or a single nucleic acid sequence for product claims for initial examination and cites M.P.E.P. 803.02. M.P.E.P. 803.02 states that "it is improper for the Office to refuse to examine that which applicants regard as their invention, unless the subject matter lacks unity of invention...Unity of invention exists where compounds included within a Markush group (1) share a common utility, and (2) share a substantial structural feature disclosed as being essential to that utility."

In the present case, all of the SEQ ID NOS share a common utility, namely their use for detecting and/or typing *H. pylori*, and all are derived from *vacA* gene, and thus share a substantial structural feature essential to the utility. Sequences derived from *vacA* have a specific utility for the detecting and/or typing of *H. pylori* which is not a general characteristic of *H. pylori* genes. That is, not all *H. pylori* genes can be used for detecting and/or typing. In view of the above argument, Applicants respectfully request reconsideration and withdrawal of the election of species requirement and examination of all of the sequences listed in claims 4, 9-10, 14, and 20-23.

Alternatively, Applicants request that the Examiner consider examination of SEQ ID NOS: 2-11 and 28-39, which are the probes of claims 20 and 22 (second alternative). Claims 4, 9 and 10 also read on these species. All of these SEQ ID NOS clearly share a common utility, namely their use for detecting and/or typing *H. pylori*, and all are derived from *vacA* gene, and thus share a substantial structural feature essential to the utility.

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As a third alternative, Applicants request that the Examiner consider examination of SEQ ID NOS: 2-7, 28-29, 35-39, and 126-149. All of these SEQ ID NOS share a common utility, namely their use for detecting and/or typing *H. pylori*, and all are derived from *vacA* gene, and thus share a substantial structural feature essential to the utility. Furthermore, these sequences are even more strongly related as they are all derived from the s-region. Typing in this region correlates with peptic ulcerations (see specification at page 2, lines 3-4). Claims 4, 9-10, 14, 20 and 22 read on this species.

As a fourth alternative, Applicants request that the Examiner consider examination of SEQ ID NOS: 126-146. All of these SEQ ID NOS share a common utility, namely their use for detecting and/or typing *H. pylori*, and all are derived from the *vacA* gene, and thus share a substantial structural feature essential to the utility. Furthermore, these sequences are even more strongly related as they are all derived from the s-region and represent a new variant, *slc*, which is described in the present specification at page 15, lines 25-31. Claims 14 reads on this species.

As a fifth alternative for the Examiner's consideration, Applicants submit 8 sequences for election: SEQ ID NOS: 2-7 and 28-29. Claims 9-10, 20 and 22 read on these sequences. All of these SEQ ID NOS share a common utility, namely their use for detecting and/or typing *H. pylori*, and all are derived from *vacA* gene, and thus share a substantial structural feature essential to the utility. Furthermore, these sequences are even more strongly related as they are all derived from the s-region. Applicants submit that these 8 sequences have unity of invention. However, even if these sequences do not have unity of invention, search and examination of the listed claims with regard to these 8 sequences can be made without a serious burden. Thus, it is proper for the Examiner to examine claims 9-10, 20 and 22 with respect to SEQ ID NOS: 2-7 and 28-29 (M.P.E.P. 803.02).

Applicants respectfully request consideration of the above arguments for the five listed alternatives. Applicants request examination of all of the sequences of Group II, or at least a fair number of sequences that can be examined without imposing an undue burden upon the Examiner.

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The fee for a four-month time extension is attached. Please charge any additional fees to our Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

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By: Che S. Chereskin

Che Swyden Chereskin
Registration No. 41,466
Agent of Record
Customer No. 20,995

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